SEQUENCE LISTING

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<110> Trotta, Christopher R.
<120> TARGETING ENZYMES OF THE tRNA SPLICING
  PATHWAY FOR IDENTIFICATION OF ANTI-FUNGAL AND/OR
  ANTI-PROLIFERATIVE MOLECULES
<130> 10589-034-999
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<141> 2004-03-26 (371c date)
<150> PCT/US2004/009590
<151> 2004-03-26
<150> 60/458,067
<151> 2003-03-27
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<213> Homo sapiens
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<223> HsSen2p
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Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly Gln Asp His Gly
Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn Asn
        3.5
Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys Gly
                        55
Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr Ile
                                        75
                    70
Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn Met
                                    90
Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala Ala
                                105
Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg Ile
                            120
Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg Asn
                        135
                                             140
Glu Glu Ala Gln Val His Asp Lys Leu Asn Ser Gly Met Val Ser Asn
Met Glu Gly Thr Ala Gly Glu Arg Pro Ser Val Val Asn Gly Asp
                                    170
Ser Gly Lys Ser Gly Gly Val Gly Asp Pro Arg Glu Pro Leu Gly Cys
                                185
Leu Gln Glu Gly Ser Gly Cys His Pro Thr Thr Glu Ser Phe Glu Lys
                            200
Ser Val Arg Glu Asp Ala Ser Pro Leu Pro His Val Cys Cys Lys
                        215
                                            220
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Gln Asp Ala Leu Ile Leu Gln Arg Gly Leu His His Glu Asp Gly Ser
                    230
                                        235
Gln His Ile Gly Leu Leu His Pro Gly Asp Arg Gly Pro Asp His Glu
                                   250
               245
Tyr Val Leu Val Glu Glu Ala Glu Cys Ala Met Ser Glu Arg Glu Ala
                               265
           260
Ala Pro Asn Glu Glu Leu Val Gln Arg Asn Arg Leu Ile Cys Arg Arg
                           280
Asn Pro Tyr Arg Ile Phe Glu Tyr Leu Gln Leu Ser Leu Glu Glu Ala
                        295
                                            300
Phe Phe Leu Val Tyr Ala Leu Gly Cys Leu Ser Ile Tyr Tyr Glu Lys
                    310
                                        315
Glu Pro Leu Thr Ile Val Lys Leu Trp Lys Ala Phe Thr Val Val Gln
                                    330
                325
Pro Thr Phe Arg Thr Thr Tyr Met Ala Tyr His Tyr Phe Arg Ser Lys
                                345
Gly Trp Val Pro Lys Val Gly Leu Lys Tyr Gly Thr Asp Leu Leu Leu
                            360
Tyr Arg Lys Gly Pro Pro Phe Tyr His Ala Ser Tyr Ser Val Ile Ile
                        375
Glu Leu Val Asp Asp His Phe Glu Gly Ser Leu Arg Arg Pro Leu Ser
                    390
                                        395
Trp Lys Ser Leu Ala Ala Leu Ser Arg Val Ser Val Asn Val Ser Lys
                405
                                    410
Glu Leu Met Leu Cys Tyr Leu Ile Lys Pro Ser Thr Met Thr Asp Lys
                                425
            420
Glu Met Glu Ser Pro Glu Cys Met Lys Arg Ile Lys Val Gln Glu Val
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                                                445
Ile Leu Ser Arg Trp Val Ser Ser Arg Glu Arg Ser Asp Gln Asp Asp
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Leu
465
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Glu Thr Tyr Glu Ser Pro Leu Pro Ile Pro Phe Gly Gln Asp His Gly
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                                25
                                                    30
Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn Asn
        35
                            40
Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys Gly
                        55
Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr Ile
                    70
                                        75
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Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn Met

Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala Ala 105 Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg Ile 120

Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg Asn

135

130

90

125

140

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Glu Glu Ala Gln Val His Asp Lys Leu Asn Ser Gly Met Val Ser Asn
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                                        155
Met Glu Gly Thr Ala Gly Gly Glu Arg Pro Ser Val Val Asn Gly Asp
                                   170
                                                       175
               165
Ser Gly Lys Ser Gly Gly Val Gly Asp Pro Arg Glu Pro Leu Gly Cys
                               185
           180
Leu Gln Glu Gly Ser Gly Cys His Pro Thr Thr Glu Ser Phe Glu Lys
       195
                          200
                                               205
Ser Val Arg Glu Asp Ala Ser Pro Leu Pro His Val Cys Cys Lys
                       215
                                          220
Gln Asp Ala Leu Ile Leu Gln Arg Gly Leu His His Glu Asp Gly Ser
                   230
                                       235
Gln His Ile Gly Leu Leu His Pro Gly Asp Arg Gly Pro Asp His Glu
               245
                                   250
Tyr Val Leu Val Glu Glu Ala Glu Cys Ala Met Ser Glu Arg Glu Ala
                               265
Ala Pro Asn Glu Glu Leu Val Gln Arg Asn Arg Leu Ile Cys Arg Arg
                           280
                                               285
Asn Pro Tyr Arg Ile Phe Glu Tyr Leu Gln Leu Ser Leu Glu Glu Glu
                       295
Pro Leu Thr Ile Val Lys Leu Trp Lys Ala Phe Thr Val Val Gln Pro
                   310
                                        315
Thr Phe Arg Thr Thr Tyr Met Ala Tyr His Tyr Phe Arg Ser Lys Gly
               325
                                    330
Trp Val Pro Lys Val Gly Leu Lys Tyr Gly Thr Asp Leu Leu Tyr
           340
                               345
Arg Lys Gly Pro Pro Phe Tyr His Ala Ser Tyr Ser Val Ile Ile Glu
                           360
                                               365
       355
Leu Val Asp Asp His Phe Glu Gly Ser Leu Arg Arg Pro Leu Ser Trp
                       375
                                            380
Lys Ser-Leu Ala Ala Leu Ser Arg Val Ser Val Asn Val Ser Lys Glu
                                        395
Leu Met Leu Cys Tyr Leu Ile Lys Pro Ser Thr Met Thr Asp Lys Glu
               405
                                   410
Met Glu Ser Pro Glu Cys Met Lys Arg Ile Lys Val Gln Glu Val Ile
                               425
Leu Ser Arg Trp Val Ser Ser Arg Glu Arg Ser Asp Gln Asp Asp Leu
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<210> 3
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<220>

<223> Sc Sen2p

<400> 3

 Met
 Ser
 Lys
 Gly
 Arg
 Val
 Asn
 Gln
 Lys
 Arg
 Tyr
 Lys
 Tyr
 Pro
 Leu
 Pro

 Ile
 His
 Pro
 Val
 Asp
 Asp
 Leu
 Pro
 Glu
 Leu
 Ile
 Leu
 His
 Asn
 Pro
 Leu

 Ser
 Trp
 Leu
 Tyr
 Arg
 Tyr
 Tyr
 Lys
 Ser
 Thr
 Asn
 Ala
 Leu

 Asn
 Asp
 Lys
 Val
 His
 Val
 Asp
 Phe
 Ile
 Gly
 Asp
 Thr
 Thr
 Leu
 His
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 Thr
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 Val
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 Phe
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 Gly
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 Leu
 His
 Ile
 His
 Ile

<211> 377

<212> PRT

<213> Saccharomyces cerevisiae

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Gly Thr Lys Ser Asn Thr Glu Thr Glu Met Thr Leu Glu Lys Val Thr
      115
             120
                                            125
Gln Gln Arg Arg Leu Gln Arg Leu Glu Phe Lys Lys Glu Arg Ala Lys
           135
                                        140
Leu Glu Arg Glu Leu Leu Glu Leu Arg Lys Gly Gly His Ile Asp
       150
                       155
Glu Glu Asn Ile Leu Leu Glu Lys Gln Arg Glu Ser Leu Arg Lys Phe
                    170
              165
Lys Leu Lys Gln Thr Glu Asp Val Gly Ile Val Ala Gln Gln Asp
                            185
                                                190
Ile Ser Glu Ser Asn Leu Arg Asp Glu Asp Asn Asn Leu Leu Asp Glu
                         200
                                            205
Asn Gly Asp Leu Leu Pro Leu Glu Ser Leu Glu Leu Met Pro Val Glu
                      215
Ala Met Phe Leu Thr Phe Ala Leu Pro Val Leu Asp Ile Ser Pro Ala
                  230
                                    235
Cys Leu Ala Gly Lys Leu Phe Gln Phe Asp Ala Lys Tyr Lys Asp Ile
              245
                                 250
His Ser Phe Val Arg Ser Tyr Val Ile Tyr His His Tyr Arg Ser His
                             265
Gly Trp Cys Val Arg Ser Gly Ile Lys Phe Gly Cys Asp Tyr Leu Leu
       275
                         280
Tyr Lys Arg Gly Pro Pro Phe Gln His Ala Glu Phe Cys Val Met Gly
                      295
                                         300
Leu Asp His Asp Val Ser Lys Asp Tyr Thr Trp Tyr Ser Ser Ile Ala
                  310
                                     315
Arg Val Val Gly Gly Ala Lys Lys Thr Phe Val Leu Cys Tyr Val Glu
              325
                                 330
Arg Leu Ile Ser Glu Gln Glu Ala Ile Ala Leu Trp Lys Ser Asn Asn
           340
                             345
Phe Thr Lys Leu Phe Asn Ser Phe Gln Val Gly Glu Val Leu Tyr Lys
       355
                          360
Arg Trp Val Pro Gly Arg Asn Arg Asp
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<212> PRT

<213> Artificial Sequence

<220>

<223> Motif

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Tyr Arg Gly Gly Tyr

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